Submitter Name: Arpana Agrawal Submitter email: arpana@wustl.edu

## An Update from the Psychiatric Genomics Consortium's Substance Use Disorder Working Group (PGC-SUD)

Arpana Agrawal<sup>1</sup>, Howard J. Edenberg<sup>2</sup>, Joel Gelernter<sup>3</sup>

<sup>1</sup>Psychiatry, Washington University School of Medicine; <sup>2</sup>Medical and Molecular Genetics, and Biochemistry and Molecular Biology, Indiana University School of Medicine; <sup>3</sup>Psychiatry, Genetics, and Neuroscience, Yale School of Medicine

PGC-SUD conducts GWAS of alcohol, cannabis, opioid and other drug use disorders. Our recent GWAS of cannabis use disorder identified 2 genome-wide significant loci, and found associations with brain volume in drug-naïve children and many mental and somatic health conditions. Consistent with prior distinctions between alcohol consumption and use disorder, cannabis use and use disorder showed opposing genetic correlations with educational attainment and BMI, but not schizophrenia or socio-economic status. We identified a consistent genetic factor structure underlying alcohol, tobacco, cannabis and opioid misuse, and conducted a large cross-SUD GWAS to identify novel loci with pleiotropic effects across multiple drugs. Findings from numerous cross-disorder GWAS have illuminated the genetic relationship between alcohol and substance use disorders, and numerous psychiatric traits. We have also undertaken rigorous examination of a proposed OUD personalized medicine approach that we demonstrated to be ill-conceived. These findings and widespread sharing of summary statistics as well as custom curation of geneand transcriptome-based analyses of SUD GWAS have cemented collaborations with addiction researchers engaged in neuroimaging and cross-species data integration. Future directions include anticipated increases in sample size via coordinated efforts aimed at harmonizing clinical, electronic health record and self-report screener data using genetically informed methods. A new sub-group has been established to conduct meta-analyses of epigenomic data. Accelerating genetic discoveries in samples of African, Asian, and LatinX origin is a priority for the SUD working group – we are one of few PGC groups to routinely conduct trans-ancestral analyses.